

1 60

61  
GTGGAAGCAATTGCGGCTTACACCCCGTGTCTTAAATACGACTTTTAAACGCCAGTGA  
-----+-----+-----+-----+-----+-----+-----+  
CACCTTCGTTAACGCCGAATGTGGGGCAACGAAATATGCTGAAAATTGCGGCACCT  
ValGluAlaIleAlaAlaTyrThrProValAlaLeuIleArgLeuLeuAsnAlaSerGly  
V E A I A A Y T P V A L I R L L N A S G  
120

121 CCTTTGCAACCTGGTCACCGTGTGGACATCGCTGATGCCAGAACGCAATTACACCGTGGGA  
-----+-----+-----+-----+-----+-----+  
GGAACGTTGGACACAGTGGCACACCTGTAGCGACTACGGTCTTCGTAATGTGGCACCCCT  
ProLeuGlnProGlyHisArgValAspIleAlaAspAlaArgSerIleTyrThrValGly  
P L Q P G H R V D I A D A R S I Y T V G

181 GCCGGGCCAGTGCCGCGGTGCACGCGCTAACCATTAATGCAAATACGATACGCCGAACG  
-----+-----+-----+-----+-----+-----+-----+  
CGCGCCGGTCACGGCGCACGTGCGGATTGGTATTACGTTTATGCTATGCGGCTTGC  
AlaAlaSerAlaAlaArgAlaArgAlaAsnHisAsnAlaAsnThrIleArgArgThr  
A A A S A A R A R A R A N H N A N T I R R T

241  
GCCATGTTGCCGAGACTGACCCCTATGACATGGTTAAGACCAACGGTTGGCTTAAACGTT  
-----+-----+-----+-----+-----+-----+-----+  
CGGTACAAACGGCTCTGACTGGGATCTGTACCAATCTGGTTGCCAACCGAATTTGCA  
AlaMetPheAlaGluThrAspProMetThrTrpLeuArgProThrValGlyLeuLysArg  
A M F A A E T D P M T W L R P P T V G L K R

FIG. 1(b)

301 ACGTTTAACCCGCGTATTATACGACCACAAACCCCAATCCATCCATGAGTTTGGAATC  
-----+-----+-----+-----+-----+-----+  
TGCAAAATTGGCGCATATAATGCTGGTGTGGGGTTAGGTAGTACTCAAACCCCTTAG  
ThrPheAsnProArgIleIleArgProGlnProProAsnProSerMetSerLeuGlyIle  
T F N P R I I R P Q P P N P S M S L G I  
360

361 TCGGGCCCTACTATATGCCGCAAAAACACAGAGCGCCGATCAGTCTGCTTTACAACAG  
-----+-----+-----+-----+-----+-----+  
AGCCCCGGATGATATAACGCGCTTTTGTGTCTCGCGCTAGTCAGACGAAATGTTGTC  
SerGlyProThrIleLeuProGlnLysThrGlnSerAlaAspGlnSerAlaLeuGlnGln  
S G P T I L P Q K T Q S A D Q S A L Q Q  
370

421 CCCGCCGCGTTGGCGTTTTCGGGATCATCCCCCGCAACACCCCCCCTCAACACGACGTCG  
-----+-----+-----+-----+-----+-----+  
GGCGCGCAACCGCAAAAGCCCTAGTAGGGCGTGTGGGGGTGGAGTTGCTGCAGC  
ProAlaAlaLeuAlaPheSerGlySerSerProGlnHisProProGlnThrThrSer  
P A A L A F S S S P Q H P P P P Q T T S  
430

481 GCATCCGTTGGACAACAGCAACACGTTGGTGTCTGGGGGTCTTCTGGACAACAACCGCAACAG  
-----+-----+-----+-----+-----+-----+  
CGTAGGCAACCTGTTGTCGTTGTGCACCAACAGCCCCCAGAACCTGTTGTCGCTGTC  
AlaSerValGlyGlnGlnGlnHisValValSerGlySerSerGlyGlnGlnProGlnGln  
A S V G Q Q Q H V V S G S S G Q Q P Q Q  
490

541 GGAGCACAGTCAAGCACTGTCCAGCCCAACAACCGGATCACCGCCCGGCCCAAGCGGTG  
-----+-----+-----+-----+-----+-----+  
CCTCGTGTACGTTGACAGTTCGGTTGTTGGCTAGTGGCGGCGCGGTTCCGCAC  
GlyAlaGlnSerSerThrValGlnProThrThrGlySerProProAlaAlaGlnGlyVal  
G A Q S S T V Q P T T G S P P A A Q G V  
550

FIG. 1(c)

```
601 CCACAGTCTACCCCGCCCCCAACCCAAATAACCCCCAGGGGGTAAGGACAGACCTTG
-----+-----+-----+-----+-----+-----+
GGTGCAGATGGGCGGGGTTGGGTTTATGGGGGTCCCCCATTCCTGTCTGGAAC
ProGlnSerThrProProProThrGlnAsnThrProGlnGlyGlyLysGlyGlnThrLeu
P Q S T P P P T Q N T P Q G G K G Q T L

661 TCACACACGGGACAAATCTGGAAACGCTTCAAGAAGTCGTAGGGTG
-----+-----+-----+-----+-----+-----+
AGTGTGTCCTGTAGACCTTTGCGAAGTTCTTCAGCATCCCAC
SerHisThrGlyGlnSerGlyAsnAlaSerArgSerArgVal
S H T G Q S G N A S R S R R V

705
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**IMMUNOREACTIVE PROTEIN VP26**  
**AND ITS DIAGNOSTIC USE**  
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**FIG. 2**

NO.	STATUS	ELISA IgM REF- ERENCE	ELISA IgM pMal- VP26* 1µm/ml	ELISA IgM pQE- VP26* 1µg/ml	NO.	STATUS	ELISA IgM REF- ERENCE	ELISA IgM pMal- VP26* 1µm/ml	ELISA IgM pQE- VP26* 1µg/ml
		CONJ. 1:50	CONJ. 1:50	CONJ. 1:25			CONJ. 1:50	CONJ. 1:50	CONJ. 1:25
		SERUM 1:42	SERUM 1:168	SERUM 1:168			SERUM 1:42	SERUM 1:168	SERUM 1:168
1	-	11	86	62	29	-	16	19	104
2	-	22	38	100	30	-	8	13	44
3	-	16	31	72	31	-	3	23	47
4	-	57	23	88	32	-	50	23	101
5	+	133	399	88	33	-	9	32	117
6	-	0	161	118	34	+	250	187	204
7	-	10	28	77	35	+	291	1079	470
8	-	47	45	60	36	-	26	52	44
9	-	7	16	63	37	+	139	66	123
10	+	132	173	160	38	-	38	87	49
11	-	71	117	70	39	-	26	25	40
12	-	0	32	75	40	-	49	13	63
13	-	17	75	66	41	-	5	20	34
14	-	11	16	57	42	-	27	43	80
15	-	23	27	73	43	-	51	49	161
16	-	11	27	59	44	-	8	38	100
17	+	979	1720	532	45	-	21	38	133
18	-	9	18	44	46	-	10	33	82
19	-	34	30	71	47	-	29	18	35
20	+	293	630	215	48	-	30	66	97
21	+	126	139	259	49	-	21	35	97
22	-	61	277	169	50	-	56	64	82
23	+	292	808	154	51	-	5	40	56
24	+	581	98	115	52	-	97	55	37
25	+	321	821	304	53	-	2	19	35
26	+	509	519	375	54	-	31	21	39
27	+	298	>2500	694					
28	-	29	36	29					

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**FIG. 3**

NO.	STATUS	ELISA IgG REF- ERENCE	ELISA IgG pMal- VP26* 1µm/ml	ELISA IgG pQE- VP26* 2µg/ml	NO.	STATUS	ELISA IgG REF- ERENCE	ELISA IgG pMal- VP26* 1µm/ml	ELISA IgG pQE- VP26* 2µg/ml
		CONJ. 1:50	CONJ. 1:50	CONJ. 1:50			CONJ. 1:50	CONJ. 1:50	CONJ. 1:50
		SERUM 1:231	SERUM 1:100	SERUM 1:100			SERUM 1:231	SERUM 1:100	SERUM 1:100
1	+	1014	176	137	28	+	549	89	172
2	+	302	87	356	29	-	34	87	120
3	+	642	97	314	30	-	76	55	128
4	+	612	87	0	31	-	0	38	101
5	+	1383	181	215	32	-	41	94	116
6	+	930	132	118	33	-	8	147	177
7	+	653	39	145	34	+	1315	860	340
8	+	915	47	469	35	+	1629	282	187
9	+	570	23	220	36	+	469	218	287
10	+	1770	131	253	37	+	693	181	346
11	+	990	104	76	38	+	1449	296	169
12	+	698	227	335	39	+	1139	85	193
13	+	141	62	501	40	+	1509	64	118
14	+	338	39	44	41	+	457	110	159
15	+	556	113	246	42	+	343	304	545
16	+	791	45	423	43	+	1455	511	244
17	+	2982	264	258	44	+	1030	174	245
18	+	1205	192	295	45	+	528	50	184
19	+	694	80	100	46	+	510	161	353
20	+	1143	270	340	47	+	300	94	290
21	+	1405	377	256	48	+	490	91	157
22	+	539	42	72	49	+	888	348	277
23	+	2449	533	530	50	+	1301	83	195
24	+	1923	1117	620	51	+	704	247	139
25	+	1420	95	54	52	+	2523	2325	757
26	PRIMARY	1194	277	66	53	+	447	99	153
	+				54	+	848	149	167
27	ZOSTER	2087	341	204					
	+								

## Figure 1(a)

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Figure 1(b)

```

ACGTTTAAACCCGCTATTATACGACCAACACCCCAATCCATCCATGAGTTTGGGAATC
301 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 360
TGCAAATTGGGGCCATAATATGCTGCTGTTGGGGGTTTAGGTAGGTACTCAAACCTTAG
ThrPheAsnProArgIleIleArgProGlnProProAsnProSerMetSerLeuGlyIle
T: P N P R I I R P Q P P N P S M S L G I

TCGGGGCTACTATATTGCCGCAAAAACACAGAGCGCGATCAGTCTGCTTTACACAG
361 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 420
AGCCCCGGATGATATAACGGCGTTTTTTTGTGTCTGGCGGCTAGTCAGACGAAATGTTGTC
SerGlyProThrIleLeuProGlnLysThrGlnSerAlaAspGlnSerAlaLeuGlnGln
S G P T I L P Q K T Q S A D Q S A L Q Q

CCCCCGCGTTGGCGTTTTTCGGGATCATCCCCGCAACCCCCCAGCTCAAACGACGTGG
421 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 480
GGCGCGCGCAACCGCAAAAGCCCTAGTAGGGCGCTTGTGGGGGTGGAGTTTGTCTGCAGC
ProAlaAlaLeuAlaPheSerGlySerSerProGlnHisProProProGlnThrThrSer
P A A L A F S G S S P Q H P P P Q T T S

GCATCGGTTGGACAACAGCAACACGTCGTGTCTGGGGTCTTCTGGACAACACCGCAACAG
481 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 540
CGTAGGCAACCTGTGTGCTTGTGCACCACAGCCCAGAAACCTGTGTGTGGCGTTGTC
AlaSerValGlyGlnGlnGlnHisValValSerGlySerSerGlyGlnGlnProGlnGln
A S V G Q Q Q H V V S G S S G Q Q P Q Q

GGAGCAGACTCAAGCACTGTCCAGCCAACAACCGATCACCGCCCGGGCCCAAGGCGTG
541 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 600
CCTCGTGTCACTTCGTGACAGGTGGGTGTTGGCTTAGTGGGGGGCCCGGGTTCCCGCAC
GlyAlaGlnSerSerThrValGlnProThrThrGlySerProProAlaAlaGlnGlyVal
G A Q S S T V Q P T T G S P P A A Q G V
  
```

0387440-060601

0273-0966

CCACAGTCTACCCCGCCCCCAACCCAAATAACCCCCGAGGGGGGTAAAGGGACAGACCTTG  
601 -----+-----+-----+-----+-----+-----+-----+  
GGTGTGAGATGGGGCGGGGGTTCGGTTTATGGGGGTCCCCCATTCCTGTCTGGAAC  
ProGlnSerThrProProProThrGlnAsnThrProGlnGlyGlyLysGlyGlnThrLeu  
P; Q S T P P P T Q N T P Q G G K G Q T L

TCACACGGGACAACTCGGAACGCTTCAGAAGTGTAGGGTG  
661 -----+-----+-----+-----+-----+-----+-----+ 705  
AGTGTGTGCCCTGTTAGACCTTTGCGAAGTCTCTCAGCATCCAC  
SerHisThrGlyGlnSerGlyAsnAlaSerArgSerArgArgVal  
S H T G Q S G N A S R S R R V



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Met Thr Gln Pro Ala Ser Ser Arg Val Val Phe Asp Pro Ser Asn Pro  
Thr Thr Phe Ser Val Glu Ala Ile Ala Ala Tyr Thr Pro Val Ala Leu  
Ile Arg Leu Leu Asn Ala Ser Gly Pro Leu Gln Pro Gly His Arg Val  
Asp Ile Ala Asp Ala Arg Ser Ile Tyr Thr Val Gly Ala Ala Ala Ser  
Ala Ala Arg Ala Arg Ala Asn His Asn Ala Asn Thr Ile Arg Arg Thr  
Ala Met Phe Ala Glu Thr Asp Pro Met Thr Trp Leu Arg Pro Thr Val  
Gly Leu Lys Arg Thr Phe Asn Pro Arg Ile Ile Arg Pro Gln Pro Pro  
Asn Pro Ser Met Ser Leu Gly Ile Ser Gly Pro Thr Ile Leu Pro Gln  
Lys Thr Gln Ser Ala Asp Gln Ser Ala Leu Gln Gln Pro Ala Ala Leu  
Ala Phe Ser Gly Ser Ser Pro Gln His Pro Pro Pro Gln Thr Thr Ser  
Ala Ser Val Gly Gln Gln Gln His Val Val Ser Gly Ser Ser Gly Gln  
Gln Pro Gln Gln Gly Ala Gln Ser Ser Thr Val Gln Pro Thr Thr Gly  
Ser Pro Pro Ala Ala Gln Gly Val Pro Gln Ser Thr Pro Pro Pro Thr  
Gln Asn Thr Pro Gln Gly Gly Lys Gly Gln Thr Leu Ser His Thr Gly  
Gln Ser Gly Asn Ala Ser Arg Ser Arg Arg Val ?

0967140-060601

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Figure 3

No.	Status	ELISA	ELISA	ELISA	No.	Status	ELISA	ELISA	ELISA
		IgM	IgM	IgM			IgM	IgM	IgM
		Reference	pMal- VP26*	pQE- VP26*			Reference	pMal- VP26*	pQE- VP26*
			1 µg/ml	1 µg/ml				1 µg/ml	1 µg/ml
		Conj.	Conj.	Conj.			Conj.	Conj.	Conj.
		1:50	1:50	1:25			1:50	1:50	1:25
		Serum	Serum	Serum			Serum	Serum	Serum
		1:42	1:168	1:168			1:42	1:168	1:168
1	-	11	86	62	29	-	16	19	104
2	-	22	38	100	30	-	8	13	44
3	-	16	31	72	31	-	3	23	47
4	-	57	23	88	32	-	50	23	101
5	+	133	399	88	33	-	9	32	117
6	-	0	161	118	34	+	250	187	204
7	-	10	28	77	35	+	291	1079	470
8	-	47	45	60	36	-	26	52	44
9	-	7	16	63	37	+	139	66	123
10	+	132	173	160	38	-	38	87	49
11	-	71	117	70	39	-	26	25	40
12	-	0	32	75	40	-	49	13	63
13	-	17	75	66	41	-	5	20	34
14	-	11	16	57	42	-	27	43	80
15	-	23	27	73	43	-	51	49	161
16	-	11	27	59	44	-	8	38	100
17	+	979	1720	532	45	-	21	38	133
18	-	9	18	44	46	-	10	33	82
19	-	34	30	71	47	-	29	18	35
20	+	293	630	215	48	-	30	66	97
21	+	126	139	259	49	-	21	35	97
22	-	61	277	169	50	-	56	64	82
23	+	292	808	154	51	-	5	40	56
24	+	581	98	115	52	-	97	55	37
25	+	321	821	304	53	-	2	19	35
26	+	509	519	375	54	-	31	21	39
27	+	298	>2500	694					
28	-	29	36	29					

109090-0444860

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**IMMUNOREACTIVE PROTEIN VP26**  
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Figure 4

No.	Status	ELISA	ELISA	ELISA	No.	Status	ELISA	ELISA	ELISA
		IgG	IgG	IgG			IgG	IgG	IgG
		Reference	pMal	pQE			Reference	pMal	pQE
			VP26*	VP26*				VP26*	VP26*
			1 µg/ml	2 µg/ml				1 µg/ml	2 µg/ml
		Conj.	Conj.	Conj.			Conj.	Conj.	Conj.
		1:50	1:50	1:50			1:50	1:50	1:50
		Serum	Serum	Serum			Serum	Serum	Serum
		1:231	1:100	1:100			1:231	1:100	1:100
1	+	1014	176	137	28	+	549	89	172
2	+	302	87	356	29	-	34	87	120
3	+	642	97	314	30	-	76	55	128
4	+	612	87	0	31	-	0	38	101
5	+	1383	181	215	32	-	41	94	116
6	+	930	132	118	33	-	8	147	177
7	+	653	39	145	34	+	1315	860	340
8	+	915	47	469	35	+	1629	282	187
9	+	570	23	220	36	+	469	218	287
10	+	1770	131	253	37	+	693	181	346
11	+	990	104	76	38	+	1449	296	169
12	+	698	227	335	39	+	1139	85	193
13	+	141	62	501	40	+	1509	64	118
14	+	338	39	44	41	+	457	110	159
15	+	556	113	246	42	+	343	304	545
16	+	791	45	423	43	+	1455	511	244
17	+	2982	264	258	44	+	1030	174	245
18	+	1205	192	295	45	+	528	50	184
19	+	694	80	100	46	+	510	161	353
20	+	1143	270	340	47	+	300	94	290
21	+	1405	377	256	48	+	490	91	157
22	+	539	42	72	49	+	888	348	277
23	+	2449	533	530	50	+	1301	83	195
24	+	1923	1117	620	51	+	704	247	139
25	+	1420	95	54	52	+	2523	2325	757
26	Primary	1194	277	66	53	+	447	99	153
	+				54	+	848	149	167
27	Zoster	2087	341	204					
	+								

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AND ITS DIAGNOSTIC USE**  
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Figure 5

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Dade Behring Marburg GmbH
- (B) STREET: Emil-von-Behring Str. 76
- (C) CITY: Marburg
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP): 35001 Marburg
- (G) TELEPHONE: 06421/39-2332
- (H) TELEFAX: 06421/39-3631

- (ii) TITLE OF INVENTION: Immunreaktives Protein VP26 des  
Varicella-Zoster-Virus (VZV) und seine diagnostische  
Verwendung

(iii) NUMBER OF SEQUENCES: 8

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: DE 19757765.2

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Varicella-Zoster-Virus
- (B) STRAIN: Ellen

(vii) IMMEDIATE SOURCE:

- (B) CLONE: VP26

(viii) POSITION IN GENOME:

- (B) MAP POSITION: ORF23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Thr Gln Pro Ala Ser Ser Arg Val Val Phe Asp Pro Ser Asn Pro

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1            5            10            15  
Thr Thr Phe Ser Val Glu Ala Ile Ala Ala Tyr Thr Pro Val Ala Leu  
20            25            30  
Ile Arg Leu Leu Asn Ala Ser Gly Pro Leu Gln Pro Gly His Arg Val  
35            40            45  
Asp Ile Ala Asp Ala Arg Ser Ile Tyr Thr Val Gly Ala Ala Ala Ser  
50            55            60  
Ala Ala Arg Ala Arg Ala Asn His Asn Ala Asn Thr Ile Arg Arg Thr  
65            70            75            80  
Ala Met Phe Ala Glu Thr Asp Pro Met Thr Trp Leu Arg Pro Thr Val  
85            90            95  
Gly Leu Lys Arg Thr Phe Asn Pro Arg Ile Ile Arg Pro Gln Pro Pro  
100            105            110  
Asn Pro Ser Met Ser Leu Gly Ile Ser Gly Pro Thr Ile Leu Pro Gln  
115            120            125  
Lys Thr Gln Ser Ala Asp Gln Ser Ala Leu Gln Gln Pro Ala Ala Leu  
130            135            140  
Ala Phe Ser Gly Ser Ser Pro Gln His Pro Pro Pro Gln Thr Thr Ser  
145            150            155            160  
Ala Ser Val Gly Gln Gln Gln His Val Val Ser Gly Ser Ser Gly Gln  
165            170            175  
Gln Pro Gln Gln Gly Ala Gln Ser Ser Thr Val Gln Pro Thr Thr Gly  
180            185            190  
Ser Pro Pro Ala Ala Gln Gly Val Pro Gln Ser Thr Pro Pro Pro Thr  
195            200            205  
Gln Asn Thr Pro Gln Gly Gly Lys Gly Gln Thr Leu Ser His Thr Gly  
210            215            220  
Gln Ser Gly Asn Ala Ser Arg Ser Arg Arg Val  
225            230            235

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

09874340-060601

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38137-0018

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Varicella-Zoster-Virus  
(B) STRAIN: Ellen

(viii) POSITION IN GENOME:

- (B) MAP POSITION: ORF23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATGACACAAC CCGCATCGTC TCGTGTAGTC TTTGATCCCA GCAACCCAC  
CACATTTTCG 60

GTGGAAGCAA TTGCGGCTTA CACCCCGTT GCTTTAATAC GACTTTTAA  
CGCCAGTGGA 120

CCTTTGCAAC CTGGTCACCG TGTGGACATC GCTGATGCCA GAAGCATTTA  
CACCGTGGGA 180

GCCGCGGCCA GTGCCGCGC TGCACGCGCT AACCATAATG CAAATACGAT  
ACGCCGAACG 240

GCCATGTTTG CCGAGACTGA CCCTATGACA TGGTTAAGAC CAACGGTTGG  
CTTAAACGT 300

ACGTTTAACC CGCGTATTAT ACGACCACAA CCCCCTAATC CATCCATGAG  
TTTGGGAATC 360

TCGGGGCCTA CTATATTGCC GCAAAAAACA CAGAGCGCCG ATCAGTCTGC  
TTTACAACAG 420

CCCGCCGCGT TGGCGTTTTC GGGATCATCC CCGCAACACC CCCCACCTCA  
AAGGACGTCG 480

GCATCCGTTG GACAACAGCA ACACGTGGTG TCGGGGTCTT CTGGACAACA  
ACCGCAACAG 540

GGAGCACAGT CAAGCACTGT CCAGCCAACA ACCGGATCAC CGCCCGCGGC  
CCAAGGCGTG 600

CCACAGTCTA CCCC GCCCCC AACCCAAAAT ACCCCCAGG GGGGTAAGGG  
ACAGACCTTG 660

TCACACACGG GACAATCTGG AAACGCTTCA AGAAGTCGTA GGGTG  
705

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

1060601-044409090

Markus EICKMANN *et al*  
**VARICELLA ZOSTER VIRUS (VZV)  
IMMUNOREACTIVE PROTEIN VP26  
AND ITS DIAGNOSTIC USE**  
38137-0018

(A) DESCRIPTION: /desc = "Synthetische DNA"

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Varicella-Zoster-Virus

(B) STRAIN: Ellen

(viii) POSITION IN GENOME:

(B) MAP POSITION: ORF23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GGAATTCGG ATGACACAAC CCGCATCGTC TCGTGTA

37

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetische DNA"

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Varicella-Zoster-Virus

(B) STRAIN: Ellen

(viii) POSITION IN GENOME:

(B) MAP POSITION: ORF23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GCTCTAGATT ACACCCTACG ACTTCTTGAA GCGTTTCC

38

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetische DNA"

(iii) HYPOTHETICAL: NO

0987440-060601

Markus EICKMANN *et al*  
**VARICELLA ZOSTER VIRUS (VZV)**  
**IMMUNOREACTIVE PROTEIN VP26**  
**AND ITS DIAGNOSTIC USE**  
38137-0018

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Varicella-Zoster-Virus

(B) STRAIN: Ellen

(viii) POSITION IN GENOME:

(B) MAP POSITION: ORF23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GGAATTCCGC GCCTGCAGGT CGACACTAGT GGAT

34

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetische DNA"

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Varicella-Zoster-Virus

(B) STRAIN: Ellen

(viii) POSITION IN GENOME:

(B) MAP POSITION: ORF23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GCTCTAGATT ACACCCTACG ACTTCTTGAA GCGTTTCC

38

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Synthetische DNA"

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Varicella-Zoster-Virus

(B) STRAIN: Ellen

09874140-060601



09-10-06-01

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

27

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(viii) POSITION IN GENOME:

(B) MAP POSITION: ORF23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

38

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